

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2002, 09:41:26 ; Search time 517.9 Seconds
(without alignments)
5944.058 Million cell updates/sec

Title: US-09-719-017a-2

Perfect score: 1793

Sequence: 1 gattccctgtgcacatca.....caattactcatgcgcgcg 1793

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_032802:*

1: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1990.DAT:*
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14: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	1793	100.0	1793	21	AAA47190	Nucleotide sequence
2	1793	100.0	1793	21	AAZ45325	Nucleotide sequence
3	1126.4	62.8	1727	15	AA086279	Nitrlilase enzyme C
4	954.2	53.2	1071	21	AAA12173	A. fecalis nitrlil
5	404	22.5	5096	16	AA083824	Plasmid pKK232-8.
6	404	22.5	5110	16	AA083833	Plasmid pCM-B64.
7	404	22.5	5110	16	AA083834	Plasmid pCM-p1208
8	404	22.5	5110	16	AA083835	Plasmid pCM-p1031
9	404	22.5	5110	16	AA083836	Plasmid pCM-T221.

10	404	22.5	5110	16	AA083825	Plasmid pcm-x# S
11	404	22.5	5110	16	AA083826	Plasmid pcm-x# 1
12	404	22.5	5110	16	AA083827	Plasmid pcm-T297
13	404	22.5	5110	16	AA083828	Plasmid pcm-p1160
14	404	22.5	5110	16	AA083829	Plasmid pcm-T270
15	404	22.5	5110	16	AA083830	Plasmid pcm-p1087
16	404	22.5	5110	16	AA083831	Plasmid pcm-p1198
17	404	22.5	5110	16	AA083832	Plasmid pcm-T286
18	403.6	22.5	502	16	AA092246	rrnB ribosomal RNA
19	401.6	22.4	7615	20	AA083833	Telomerase coding
20	401.6	22.4	7688	20	AA083834	Telomerase coding
21	401.6	22.4	7797	20	AA083835	Telomerase coding
22	388.4	21.7	4222	10	AA092038	Sequence of recomb
23	388.4	21.7	4466	10	AA092038	Sequence of recomb
24	388.4	21.7	4466	15	AA086637	pT104-4 sequence
25	386.8	21.6	4207	10	AA092031	Sequence of recomb
26	385.2	21.5	4204	12	AA010279	Sequence of recomb
27	336	18.7	5641	22	AA030800	Vector plasmid pJM
28	336	18.7	5670	22	AA030801	Vector plasmid pJM
29	336	18.7	5826	22	AA030798	Vector plasmid pJM
30	336	18.7	6071	22	AA030799	Vector plasmid pJM
31	332.8	18.6	3753	24	ABA04129	Plasmid pHE19T(II)
32	332.8	18.6	3753	24	ABA04130	Plasmid pHE19T(II)
33	332.8	18.6	3950	22	AA081854	Plasmid pSB-92 nuc
34	332.8	18.6	4176	10	AA090709	Sequence of plasmid
35	332.8	18.6	4214	21	AA062632	Vector pEP1ink6 D
36	332.8	18.6	4214	21	AA059260	Nucleotide sequence
37	332.8	18.6	4357	22	AA031389	Expression vector
38	332.8	18.6	4816	22	AA007799	Expression vector
39	332.8	18.6	5021	21	AA007775	Expression vector
40	332.8	18.6	5027	20	AA078865	Human tissue facto
41	332.8	18.6	5069	20	AA078874	Human tissue facto
42	332.8	18.6	5069	20	AA078871	Human tissue facto
43	332.8	18.6	5099	20	AA078896	Human tissue facto
44	332.8	18.6	5104	22	AA007798	Human tissue facto
45	332.8	18.6	5132	20	AA078883	Human tissue facto

ALIGNMENTS

RESULT 1	
AAA47190	standard: DNA: 1793 BP.
AAA47190	
AC	AAA47190:
XX	
DT	03-OCT-2000 (first entry)
DE	Nucleotide sequence of the expression cassette of pRPA-BCAT41.
XX	
KW	Methionine, 2-hydroxy-4-methylthiobutanoic acid; nitrilase;
KW	nitrile hydratase; amidase; pRPA-BCAT41; ss.
XX	
OS	Synthetic.
XX	
FT	Key location/Qualifiers
FT	123..1193
FT	CDS /**tag= a
PN	WO200036120-A1.
PD	22-JUN-2000.
PF	10-DEC-1999; 99WO-FR03089.
PR	11-DEC-1998; 98FR-0015849.
PR	19-JUL-1999; 99FR-0009489.
PA	(RHON) RHONE-POULENC ANIMAL NUTRITION SA.
XX	
PI	Favre-Bulle O, Pierrard J, Batisse Deblitte N;

Oy 1741 gctcagcattgtatgtgtccgaagcgaacaacattactcaatgccgcg 1793
Db 1741 gctcagcattgtatgtgtccgaagcgaacaacattactcaatgccgcg 1793

RESULT 2

AAZ45325
ID AAZ45325 standard; DNA; 1793 BP.

AAZ45325;

27-MAR-2000 (first entry)

Nucleotide sequence of an expression cassette encoding a nitrilase.

XX Tryptophan promoter; Prrp promoter; heterologous protein expression;
KW Escherichia coli W; industrial protein production; enzyme: nitrilase; ss.

XX Synthetic.
OS Alcaligenes faecalis.

XX Key Location/Qualifiers
FT CDS 123..1193
FT /*tag= a
FT /product= "nitrilase"

XX MO9964607-A1.

XX 16-DEC-1999.

XX 08-JUN-1999; 99WO-FR01343.

XX 10-JUN-1998; 98FR-0007474.

XX (RHON) RHONE-POULENC NUTRITION ANIMALE.

XX Pierard J, Guitton C, Favre-Bulle O;

XX WPI: 2000-097541/08.
XX P-PSDB: MAY34121.

XX Industrial production of heterologous proteins in Escherichia coli
PT strain W, particularly for expressing enzymes -

XX Example 1: Page 36-38; 52pp; French.

XX The present sequence represents an expression cassette comprising
CC the tryptophan promoter (Prrp promoter) and DNA encoding an Alcaligenes
CC faecalis ATCC8750 nitrilase (nitrB). The nitrilase polynucleotide and the
CC promoter sequence were extracted from plasmid pRP4604r6 by restriction
CC digest. The Prrp promoter is used to control the expression of a
CC heterologous protein in an expression cassette which is used to modify
CC a strain of Escherichia coli W. The modified strain is then used for
CC industrial production of heterologous proteins. Specifically, the
CC promoter is used to control the expression of an Alcaligenes nitrilase
CC gene. The method is especially used to produce proteins of relatively
CC low value, preferably enzymes and specifically nitrilases.

XX Sequence 1793 BP; 412 A; 527 C; 478 G; 376 T; 0 other;

Query Match 100.0%; Score 1793; DB 21; Length 1793;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gaattccgtgtgacaataatcgcgaactagttactagtagcagcttgcctgcag 60
Db 1 gaattccgtgtgacaataatcgcgaactagttactagtagcagcttgcctgcag 60
Oy 61 tgcagctgcagcgaagcttgggcatacatcaatcgaatgttatctgaagaatactac 120
Db 61 tgcagctgcagcgaagcttgggcatacatcaatcgaatgttatctgaagaatactac 120

Oy 121 atatgcagacaagaanaaaatcgtccgggcagccgctacagccgcctctcccaactag 180
Db 121 atatgcagacaagaanaaaatcgtccgggcagccgctacagccgcctctcccaactag 180
Oy 181 atctgcgaacgggtgtgtatataaaacattgagctgtgctcgtcgaagcccgcatgaggt 240
Db 181 atctgcgaacgggtgtgtatataaaacattgagctgtgctcgtcgaagcccgcatgaggt 240
Oy 241 gtgacctgacgtgttctgtgtaaaacctgtgcccgtctatcccttcaagctgtgcttg 300
Db 241 gtgacctgacgtgttctgtgtaaaacctgtgcccgtctatcccttcaagctgtgcttg 300
Oy 301 ggcagccgctgtgtcgtctgtaataatcagtcgccgttactatgccaactcgtctccgtg 360
Db 301 ggcagccgctgtgtcgtctgtaataatcagtcgccgttactatgccaactcgtctccgtg 360
Oy 361 acagtgcaagatttcaaacgattgccagcgccagcagaccttggtaatttcatcgcac 420
Db 361 acagtgcaagatttcaaacgattgccagcgccagcagaccttggtaatttcatcgcac 420
Oy 421 tgggtatagcagcagcagcagcggcggcagccttaccctggccaatgctctatcagaca 480
Db 421 tgggtatagcagcagcagcagcggcggcagccttaccctggccaatgctctatcagaca 480
Oy 481 agggcagatcgtgtgtcgcgttcgcaaacctcaaacctacatgtttagcgcagccgtgt 540
Db 481 agggcagatcgtgtgtcgcgttcgcaaacctcaaacctacatgtttagcgcagccgtgt 540
Oy 541 ttggtgaaggtatagcccgagatcagatgtgtccgaacacgagcttggccgctgcgttg 600
Db 541 ttggtgaaggtatagcccgagatcagatgtgtccgaacacgagcttggccgctgcgttg 600
Oy 601 cccctgtcgtcgttggagcagcactgtcccttgagcgaagtacgcgtctactcccaagc 660
Db 601 cccctgtcgtcgttggagcagcactgtcccttgagcgaagtacgcgtctactcccaagc 660
Oy 661 aagccattcacattgcgcgccttgcctcttctgtctatcagcgaagaagcccatgcgc 720
Db 661 aagccattcacattgcgcgccttgcctcttctgtctatcagcgaagaagcccatgcgc 720
Oy 721 tcaagcgaaggttgaacatgtgctgtcctgcgaatcattcgtgtgaagccagctgttta 780
Db 721 tcaagcgaaggttgaacatgtgctgtcctgcgaatcattcgtgtgaagccagctgttta 780
Oy 781 ccattgcgcgcagcagctgtctcaccagagagacacttgacatgctgtaagtatgtgac 840
Db 781 ccattgcgcgcagcagctgtctcaccagagagacacttgacatgctgtaagtatgtgac 840
Oy 841 acaagcctccctgtctgaaggtgggcgcgcgcagcttcatgattttgcgcgcgcgcgac 900
Db 841 acaagcctccctgtctgaaggtgggcgcgcgcagcttcatgattttgcgcgcgcgcgac 900
Oy 901 gacattgctcctaccctcgtccacacgaltgcgaagcctgtatcatctgacgtcgaatga 960
Db 901 gacattgctcctaccctcgtccacacgaltgcgaagcctgtatcatctgacgtcgaatga 960
Oy 961 tggagaagaatttgccttcgcgaagcgatcaaacgacctgtgtggccactactcaaaccc 1020
Db 961 tggagaagaatttgccttcgcgaagcgatcaaacgacctgtgtggccactactcaaaccc 1020
Oy 1021 aggcacccgcttctgtacttgcagccttgggcagcgcgagcccatgactcgggtgata 1080
Db 1021 aggcacccgcttctgtacttgcagccttgggcagcgcgagcccatgactcgggtgata 1080
Oy 1081 aaagcgtatccagaagaagctcccgagcgcgcagctgcgaagtacggctgcgcgcgtg 1140
Db 1081 aaagcgtatccagaagaagctcccgagcgcgcagctgcgaagtacggctgcgcgcgtg 1140
Oy 1141 ccgtacgcagactcagagactcgtatcgtactgttgcaagaacccgttcgaacccaaa 1200
Db 1141 ccgtacgcagactcagagactcgtatcgtactgttgcaagaacccgttcgaacccaaa 1200

QY 1201 agatgacaagcccgagcaactgctccggtcttgatctcttctgctccgagtcact 1260
CC |
CC |
CC |
DB 1201 agatgacaagcccgagcaactgctccggtcttgatctcttctgctccgagtcact 1260
QY 1261 agtctcgaagtcagaccgagcctgcaagcttggtgtccaccgaccgacatgcgcgact 1320
CC |
CC |
CC |
DB 1261 agtctcgaagtcagaccgagcctgcaagcttggtgtccaccgaccgacatgcgcgact 1320
QY 1321 cagaagtgaaacgcgcgtagcgcgtagtgctggtgtctccccaatgcgagatgaagga 1380
CC |
CC |
CC |
DB 1321 cagaagtgaaacgcgcgtagcgcgtagtgctggtgtctccccaatgcgagatgaagga 1380
QY 1381 actgcccagatcaataaataaagcctcagtcgaaagactgggaccttcgtttatc 1440
DB 1381 actgcccagatcaataaataaagcctcagtcgaaagactgggaccttcgtttatc 1440
QY 1441 tgtgtgtgtcgttgaaagctctccctgagtaggacaatactgcgcggagagattgaac 1500
CC |
CC |
CC |
DB 1441 tgtgtgtgtcgttgaaagctctccctgagtaggacaatactgcgcggagagattgaac 1500
QY 1501 gtctcgaaagcaacgcccggaggtggtggtgagcagagacgcccgcataaactgccaagcat 1560
DB 1501 gtctcgaaagcaacgcccggaggtggtggtgagcagagacgcccgcataaactgccaagcat 1560
QY 1561 caaatgaagcaagaagccatctcgtgagcgtatggccttttgcgtttctcaaaactctcct 1620
DB 1561 caaatgaagcaagaagccatctcgtgagcgtatggccttttgcgtttctcaaaactctcct 1620
QY 1621 gtctgcatctacaagcctcccccacagatagcgttaactagacctgttttgatc 1680
DB 1621 gtctgcatctacaagcctcccccacagatagcgttaactagacctgttttgatc 1680
QY 1681 aggaagcagcgtatgaaccactctcttaaaacccctgagacaacttggcagatgaataat 1740
DB 1681 aggaagcagcgtatgaaccactctcttaaaacccctgagacaacttggcagatgaataat 1740
QY 1741 gctcagacactgtgtgtgctcggaagacaacaatactcaatgccgcg 1793
DB 1741 gctcagacactgtgtgtgctcggaagacaacaatactcaatgccgcg 1793
RESULT 3
AA086279
ID AA086279 standard; DNA: 1727 BP.
AC AA086279;
XX
XX
DT 12-AUG-1999 (first entry)
XX
XX
DE Nitrilase enzyme coding sequence.
XX
XX
KW Nitrilase; organic acid preparation; nitrile compound hydrolysis;
KW amide production; carboxylic acid production; ss.
XX
XX
OS Alcaligenes faecalis.
XX
XX
PN JP06153968-A.
XX
XX
PD 03-JUN-1994.
XX
XX
PF 17-NOV-1992: 92JP-0306663.
XX
XX
PR 17-NOV-1992: 92JP-0306663.
XX
XX
PA (NITR) NITRO CHEM IND CO LTD.
XX
XX
DR WPI: 1994-220515/27.
XX
XX
DR P-PSDB: AAR61104.
XX
XX
PT Organic acid prepn by hydrolysing nitrile - using nitrilase enzyme
XX
XX
PS obtd from transformed organism.
PS Claim 1; Fig 2; 9pp; Japanese.

XX
CC This sequence encodes the nitrilase enzyme from *Alcaligenes faecalis*.
CC The invention relates to a method of preparing organic acid by
CC hydrolysing nitrile compounds of formula R1CH(R2)CN with nitrilase to
CC form carboxylic acid of formula R1CH(R2)COOH and equimolar amount of
CC ammonia. (R1 is optionally substituted phenyl, naphthyl, indole,
CC thiophene, pyridyl or cyclohexenyl; R2 is H or hydroxyl group). The
CC nitrilase is prepared by culturing a transformant containing recombinant
CC DNA obtained by integrating into a vector the *A. faecalis* nitrilase
CC enzyme DNA. Various kinds of amide or carboxylic acid can be produced
CC industrially in good efficiency.
SQ Sequence 1727 BP; 343 A; 566 C; 468 G; 350 T; 0 other;
Query Match 62.8%; Score 1126.4; DB 15; Length 1727;
Best Local Similarity 99.5%; Pred. No. 3,5e-234;
Matches 1130; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 122 tatgacagacaagaaaaatcgctccggcagccgcgtacagagccgctctcccaactacga 181
DB 122 tatgacagacaagaaaaatcgctccggcagccgcgtacagagccgctctcccaactacga 181
QY 182 tctggcacaaggtgttgataaaacattgagctgctgcgtcagagcccgagatgaaggtctg 241
DB 182 tctggcacaaggtgttgataaaacattgagctgctgcgtcagagcccgagatgaaggtctg 241
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DB 242 tgaacctatcgtgtttgtgaaaccttgctgcccgcgtacacctccctcaagctcgtgctgg 301
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DB 302 cgaacccgctgtgtcgtgaaatacagtgccgctactatgccaactgctctcgtctgta 361
QY 362 cagtcgaagtttccaagcattgcccagcgcgacgacctgggtattttatctgcact 421
DB 362 cagtcgaagtttccaagcattgcccagcgcgacgacctgggtattttatctgcact 421
QY 421 cagtcgaagtttccaagcattgcccagcgcgacgacctgggtattttatctgcact 421
DB 421 cagtcgaagtttccaagcattgcccagcgcgacgacctgggtattttatctgcact 421
QY 422 gggttatagcagc 481
DB 422 gggttatagcagc 481
QY 481 gggttatagcagc 481
DB 481 gggttatagcagc 481
QY 482 gggccagatgctgtgtgcgcgtcgcgaactcaaaactacaatgcttgagcgcacgtgt 541
DB 482 gggccagatgctgtgtgcgcgtcgcgaactcaaaactacaatgcttgagcgcacgtgt 541
QY 541 gggccagatgctgtgtgcgcgtcgcgaactcaaaactacaatgcttgagcgcacgtgt 541
DB 541 gggccagatgctgtgtgcgcgtcgcgaactcaaaactacaatgcttgagcgcacgtgt 541
QY 542 tggctgaaggttatgcccagatctgattgtgtcgcgaacacggaactggccggtcggtgc 601
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QY 601 tggctgaaggttatgcccagatctgattgtgtcgcgaacacggaactggccggtcggtgc 601
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DB 661 cctgtgtctgtggaagcactgtccctctgagcaagtagcgtcttaactccagacga 661
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QY 721 agccatcacatctgcgcgtcgcgtctcttctgcgtgtacagcgaaagcccatgcgt 721
DB 721 agccatcacatctgcgcgtcgcgtctcttctgcgtgtacagcgaaagcccatgcgt 721
QY 722 cagcgccaagtgaaatgctgctcctcgcaactatctggttgaaagccagtgcttac 781
DB 722 cagcgccaagtgaaatgctgctcctcgcaactatctggttgaaagccagtgcttac 781
QY 781 cagcgccaagtgaaatgctgctcctcgcaactatctggttgaaagccagtgcttac 781
DB 781 cagcgccaagtgaaatgctgctcctcgcaactatctggttgaaagccagtgcttac 781
QY 782 catcgccgcagcagtgctgtcaccccgagacacgtgacatctggaagtgaagtgaac 841
DB 782 catcgccgcagcagtgctgtcaccccgagacacgtgacatctggaagtgaagtgaac 841
QY 841 catcgccgcagcagtgctgtcaccccgagacacgtgacatctggaagtgaagtgaac 841
DB 841 catcgccgcagcagtgctgtcaccccgagacacgtgacatctggaagtgaagtgaac 841
QY 842 caacgctctcctgtgaaagtggcgcgagcttcacatgtttctgcgcgcgagcgaagc 901
DB 842 caacgctctcctgtgaaagtggcgcgagcttcacatgtttctgcgcgcgagcgaagc 901
QY 901 caacgctctcctgtgaaagtggcgcgagcttcacatgtttctgcgcgcgagcgaagc 901
DB 901 caacgctctcctgtgaaagtggcgcgagcttcacatgtttctgcgcgcgagcgaagc 901
QY 902 cacattgctcctactcgcacacagatgcggaagcgtgatatgctgcgagatgaacat 961
DB 902 cacattgctcctactcgcacacagatgcggaagcgtgatatgctgcgagatgaacat 961

Query Match	53.28;	Score 954.2;	DB 21;	Length 1071;
Best Local Similarity	93.28;	Pred. No. 5.4e-197;		
Matches 998; Conservative	0;	Mismatches 73;	Indels 0;	Gaps 0;

[illegible]

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RESULT      5
AA083824
ID   AA083824 standard; DNA; 5096 BP.
XX
AC   AA083824;
XX
DT   04-OCT-1995 (first entry)
XX
DE   Plasmid pKK232-8.
XX
KM   Plasmid pKK232-8; bacteriophage T7; RNA polymerase;
XX   mutant promoters; circular; cyclic; ds.
XX
OS   Synthetic.
XX
FH   Key
FT   misc-feature      177..212
FT                       /tag=
FT                       /note="Cloning polylinker prior to a promoterless
FT                           chloramphenicol acetyl transferase gene"
XX
PN   US5385834-A.
XX
PD   31-JAN-1995.
XX
PE   13-AUG-1993; 93US-0106433.
XX
PR   13-AUG-1993; 93US-0106433.
XX
PA   (GEOR-) GEORGIA TECH RES CORP.
XX
PI   Ikeda RA;
XX
DR   WPI; 1995-081565/11.
XX
PT   New mutant form of T7 RNA polymerase - able to utilize a wide
PT   range of T7 promoter sequences having mutations that inactivate
PT   recognition by wild type enzyme
XX
PS   Disclosure; Columns 37-42: 79pp; English.
XX
CC   AA083824 is the plasmid pKK232-8, it was used in the production of
CC   claimed bacteriophage T7 RNA polymerase mutant promoters.
XX
SQ   Sequence 5096 BP; 1294 A; 1290 C; 1290 G; 1222 T; 0 other;

Query Match      22.5%; Score 404; DB 16; Length 5096;
Best Local Similarity 96.5%; Pred. No. 4.9e-78;
Matches 413; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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DB   1537 aagcagaagcgcatcctgaagatgagcttctgcttctacaactctctgctgc 1596
      |||
QY   1627 atactcaagcgatccccccacagatacgtaactagctgttttgcatcagaag 1686
      |||
DB   1597 atactcaagcgatccccccacagatacgtaactagctgttttgcatcagaag 1656
      |||
QY   1687 gcagctat 1694
      |||
DB   1657 gcagctgt 1664
      |||

RESULT      6
AA083833
ID   AA083833 standard; DNA; 5110 BP.
XX
AC   AA083833;
XX
DT   05-OCT-1995 (first entry)
XX
DE   Plasmid PCM-B64.
XX
KM   Plasmid PCM-B64; bacteriophage T7; RNA polymerase;
XX   mutant -8T to C; T7 promoter phi 10; circular; cyclic; ds.
XX
OS   Synthetic.
XX
FH   Key
FT   Promoter          198..220
FT                       /tag=
FT                       /note="Intermediate T7 promoter phi 10 mutant (-8T
FT                           to C) prior to a promoterless chloramphenicol
FT                           acetyl transferase gene"
XX
PN   US5385834-A.
XX
PD   31-JAN-1995.
XX
PE   13-AUG-1993; 93US-0106433.
XX
PR   13-AUG-1993; 93US-0106433.
XX
PA   (GEOR-) GEORGIA TECH RES CORP.
XX
PI   Ikeda RA;
XX
DR   WPI; 1995-081565/11.
XX
PT   New mutant form of T7 RNA polymerase - able to utilize a wide
PT   range of T7 promoter sequences having mutations that inactivate
PT   recognition by wild type enzyme
XX
PS   Disclosure; Columns 97-104: 79pp; English.
XX
CC   AA083833 is the plasmid PCM-B64, it was used in the production of
CC   the bacteriophage T7 RNA polymerase mutant promoter phi 10 -8T
CC   to C substitution (claimed).
XX
SQ   Sequence 5110 BP; 1305 A; 1289 C; 1289 G; 1227 T; 0 other;

Query Match      22.5%; Score 404; DB 16; Length 5110;
Best Local Similarity 96.5%; Pred. No. 4.9e-78;
Matches 413; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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[illegible]

RESULT	7
AA083834	
ID	AA083834 standard; DNA: 5110 BP.
XX	
AC	AA083834;
XX	
DT	05-OCT-1995 (first entry)
XX	
DE	Plasmid PCM-P1208.
XX	
KW	Plasmid PCM-P1208; bacteriophage T7; RNA polymerase;
XX	mutant -7C to G; T7 promoter phi 10; circular; cyclic; ds.
OS	Synthetic.
XX	
Key	Location/Qualifiers
FT	Promoter
FT	198..220
FT	/tag= a
FT	/note= "inactive T7 promoter phi 10 mutant (-7C to
FT	G) prior to a promoterless chloramphenicol
FT	acetyl transferase gene"
XX	
PN	US5385834-A.
XX	
PD	31-JAN-1995.
XX	
PE	13-AUG-1993; 93US-0106433.
XX	
PR	13-AUG-1993; 93US-0106433.
XX	
RA	(GEOR-) GEORGIA TECH RES CORP.
XX	
PI	Ikeda RA;
XX	
DR	WPI: 1995-081565/11.
XX	
PT	New mutant form of T7 RNA polymerase - able to utilise a wide
PT	range of T7 promoter sequences having mutations that inactivate
PT	recognition by wild type enzyme
XX	
PS	Disclosure; Columns 105-110; 79pp; English.
XX	
CC	AA083834 is the plasmid PCM-P1208, it was used in the production of
CC	the bacteriophage T7 RNA polymerase mutant promoter phi 10 -7C
CC	to G substitution (claimed).
XX	
SO	Sequence 5110 BP; 1305 A; 1298 C; 1290 G; 1227 T; 0 other;

Query Match	22.5%	Score 404:	DB 16:	Length 5110:
Best Local Similarity	96.5%:	Pred. No.	4.9e-78:	
Matches 413:	Conservative	0:	Mismatches 15:	Indels 0:
Gaps	0:			
QY	1267	agagtcgacatctcgaacgatcttggtcccaactgaccatacgccaactcagaag	1326	
Db	1251	agaatttgccttgaggcagtagcgggtgtcccaactgaccatacgccaactcagaag	1310	
QY	1327	tgaaacgcgctatgcgcgatgttgtgtgtgtttcccatactgcagagttaaggactgcc	1386	
Db	1311	tgaaaacgcgttagccgcgatgttgtgtgtgtttcccatactgcagagttaaggactgcc	1370	
QY	1387	aggcatcaataaaaacgaaaggctcagtcgaaaggacttgagcttcgtttatctgtgt	1446	
Db	1371	aggcatcaataaaaacgaaaggctcagtcgaaaggacttgagcttcgtttatctgtgt	1430	
QY	1447	ttgtcgtgtgaacgctctccctgtagtgaacaataccgcgcggagacgagatttgaacgttgcc	1506	
Db	1431	ttgtcgtgtgaacgctctccctgtagtgaacaataccgcgcggagacgagatttgaacgttgcc	1490	
QY	1507	aagcaaacgccccggaggtgtgtgcgggcaggaagcccgccataactgcgcagcagcataaat	1566	
Db	1491	aagcaaacgccccggaggtgtgtgcgggcaggaagcccgccataactgcgcagcagcataaat	1550	
QY	1567	aagcaaacgccccatccctgaacgatggccttttgcgtttctiaacaacttcctgtgtgc	1626	
Db	1551	aagcaaacgccccatccctgaacgatggccttttgcgtttctiaacaacttcctgtgtgc	1610	
QY	1627	atatctacaagcacatccccccacagatacgtttaacttagcctcgtttttgtcatcaggaa	1686	
Db	1611	atatctacaagcacatccccccacagatacgtttaacttagcctcgtttttgtcatcaggaa	1670	
QY	1687	gcagcttat	1694	
Db	1671	gcagcttgt	1678	
RESULT 8				
AAO83835				
ID	AAO83835	standard; DNA;	5110 BP.	
AC	AAO83835;			
DT	06-OCT-1995	(first entry)		
DE	Plasmid PCM-P1031.			
KW	Plasmid PCM-P1031; bacteriophage T7; RNA polymerase;			
KW	mutant -7C to A; T7 promoter phi 10; circular; cyclic; ds.			
OS	Synthetic.			
FH	Key	Location/Qualifiers		
FT	Promoter	198..220		
FT	/tag=	a		
FT	/note=	"inactive T7 promoter phi 10 mutant (-7C to		
FT	A) prior to a promoterless chloramphenicol			
FT	acetyl transferase gene"			
XX	US5385834-A.			
XX	31-JAN-1995.			
XX	13-AUG-1993;	93US-0106433.		
XX	PR	13-AUG-1993;	93US-0106433.	
PA	(GEOR-) GEORGIA TECH RES CORP.			
PI	Ikeda RA;			
DR	WPI; 1995-081565/11.			

XX New mutant form of T7 RNA polymerase - able to utilise a wide
PT range of T7 promoter sequences having mutations that inactivate
PT recognition by wild type enzyme
XX
XX
XX
XX Disclosure; Columns 111-118; 79pp; English.
XX
XX AA083635 is the plasmid pCM-P1031, it was used in the production of
CC the bacteriophage T7 RNA polymerase mutant promoter phi 10 -7C
CC to A substitution (claimed).
XX
XX Sequence 5110 BP; 1306 A; 1286 C; 1290 G; 1228 T; 0 other;
XQ

Query Match	22.5%;	Score 404;	DB 16;	Length 5110;
Best Local Similarity	-96.5%;	Pred. NO. 4.9e-78;		
Matches 413; Conservative	0;	Mismatches 15;	Indels 0;	Gaps 0;

[illegible]

RESULT	9	
AAQ083836		
ID	AAQ083836	standard; DNA; 5110 bp.
XX		
AC	AAQ083836;	
XX		
DT	06-OCT-1995	(first entry)
XX		
DE	Plasmid PCM-T221.	
XX		
KW	Plasmid PCM-T221; bacteriophage T7; RNA polymerase;	
mutant	-6A to G; T7 promoter ph1 10; circular; cyclic; ds.	
XX		
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Promoter	198..220
FT		/tag= a
FT	/note=	"intermediate T7 promoter ph1 10 mutant (-6A
FT		to G) prior to a promoterless chloramphenicol
FT		acetyl transferase gene"
XX		

PN	US5385834-A.
XX	
PD	31-JAN-1995.
XX	
PF	13-AUG-1993; 93US-0106433.
XX	
PR	13-AUG-1993; 93US-0106433.
XX	
PA	(GEOR-) GEORGIA TECH RES CORP.
XX	
PI	Ikeda RA;
XX	
DR	WPI; 1995-081565/11.

Query Match	22.5%	Score 404;	DB 16;	Length 5110;
Best Local Similarity	96.5%;	Pred. No. 4.9e-78;		
Matches 413;	Conservative 0;	Mismatches 15;	Indels 0;	Gaps 0

[illegible]


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XX XX Plasmid pCM-X#; bacteriophage T7; RNA polymerase;
KM mutant promoters; circular; cyclic; ds.
XX XX Synthetic.
XX XX
XX Key Location/Qualifiers
FH Promoter 198..220
FT /tag= a
FT /note= "potential T7 promoter prior to a promoterless
FT chloramphenicol acetyl transferase gene"
XX
XX US5385834-A.
XX
XX 31-JAN-1995.
XX
XX 13-AUG-1993; 93US-0106433.
XX
XX 13-AUG-1993; 93US-0106433.
XX
XX (GEOB-) GEORGIA TECH RES CORP.
XX
XX Ikeda RA;
XX
XX WPI; 1995-081565/11.
XX
XX New mutant form of T7 RNA polymerase - able to utilise a wide
XX range of T7 promoter sequences having mutations that inactivate
XX recognition by wild type enzyme
XX
XX Disclosure; Columns 43-50; 79pp; English.
XX
XX AA083825 is the plasmid pCM-X#, it was used in the production of
XX claimed bacteriophage T7 RNA polymerase mutant promoters.
XX
XX Sequence 5110 BP; 1303 A; 1287 C; 1288 G; 1226 T; 6 other;
SQ

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Query Match 22.5%; Score 404; DB 16; Length 5110;
 Best Local Similarity 96.5%; Pred. No. 4.9e-78;
 Matches 413; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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QY 1267 agagtcgagcctgcagcgtgacgtgtccacactgacccatgcccgaactcagaag 1326
DB 1251 agaatttcctgctgcgcgtagcgcggtgtccacactgacccatgcccgaactcagaag 1310
QY 1327 tgaacgcgcgtagcgcgcgtagtggtgtgtcccatgagagtagggaactgccc 1386
DB 1311 tgaacgcgcgtagcgcgcgtagtggtgtgtcccatgagagtagggaactgccc 1370
QY 1387 aggcataataaagaagagtcagtcgaaagactggtgcttcgttttctgtgt 1446
DB 1371 aggcataataaagaagagtcagtcgaaagactggtgcttcgttttctgtgt 1430
QY 1447 ttgtcgtgaaacgctctcctgtagtagacaatcccgccggagcgagattgaaactgtgcg 1506
DB 1431 ttgtcgtgaaacgctctcctgtagtagacaatcccgccggagcgagattgaaactgtgcg 1490
QY 1507 aagcaacggcccgagaggtgtgcgagcagagcgcgcgcataaactgccaagcatcaatt 1566
DB 1491 aagcaacggcccgagaggtgtgcgagcagagcgcgcgcataaactgccaagcatcaatt 1550
QY 1567 aagcagaagcgcatactctgacgagatggtcttttgcgtttctacaacttctctgtgcgc 1626
DB 1551 aagcagaagcgcatactctgacgagatggtcttttgcgtttctacaacttctctgtgcgc 1610
QY 1627 atattacaaagcattccccacagatacagtaaacatgacctcgttttgcatacagaagaa 1686
DB 1611 atattacaaagcattccccacagatacagtaaacatgacctcgttttgcatacagaagaa 1670
QY 1687 gcaagctat 1694
DB 1671 gcaagctat 1678

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RESULT 11
AA083826
ID AA083826 standard; DNA; 5110 BP.
XX
XX AA083826;
AC
XX 04-OCT-1995 (first entry)
XX
XX Plasmid pCAT10-1.
XX
XX Plasmid pCAT10-1; bacteriophage T7; RNA polymerase;
KM mutant promoters; circular; cyclic; T7 promoter phi 10; ds.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH misc_feature 198..220
FT /tag= a
FT /note= "T7 promoter phi 10 prior to a promoterless
FT chloramphenicol acetyl transferase gene"
XX
XX US5385834-A.
XX
XX 31-JAN-1995.
XX
XX 13-AUG-1993; 93US-0106433.
XX
XX 13-AUG-1993; 93US-0106433.
XX
XX (GEOB-) GEORGIA TECH RES CORP.
XX
XX Ikeda RA;
XX
XX WPI; 1995-081565/11.
XX
XX New mutant form of T7 RNA polymerase - able to utilise a wide
XX range of T7 promoter sequences having mutations that inactivate
XX recognition by wild type enzyme
XX
XX Disclosure; Columns 51-56; 79pp; English.
XX
XX AA083826 is the plasmid pCAT10-1, it was used in the production of
XX the bacteriophage T7 RNA polymerase promoter phi 10.
XX
XX Sequence 5110 BP; 1305 A; 1288 C; 1289 G; 1228 T; 0 other;
SQ

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Query Match 22.5%; Score 404; DB 16; Length 5110;
 Best Local Similarity 96.5%; Pred. No. 4.9e-78;
 Matches 413; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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QY 1267 agagtcgagcctgcagcgtgacgtgtccacactgacccatgcccgaactcagaag 1326
DB 1251 agaatttcctgctgcgcgtagcgcggtgtccacactgacccatgcccgaactcagaag 1310
QY 1327 tgaacgcgcgtagcgcgcgtagtggtgtgtcccatgagagtagggaactgccc 1386
DB 1311 tgaacgcgcgtagcgcgcgtagtggtgtgtcccatgagagtagggaactgccc 1370
QY 1387 aggcataataaagaagagtcagtcgaaagactggtgcttcgttttctgtgt 1446
DB 1371 aggcataataaagaagagtcagtcgaaagactggtgcttcgttttctgtgt 1430
QY 1447 ttgtcgtgaaacgctctcctgtagtagacaatcccgccggagcgagattgaaactgtgcg 1506
DB 1431 ttgtcgtgaaacgctctcctgtagtagacaatcccgccggagcgagattgaaactgtgcg 1490
QY 1507 aagcaacggcccgagaggtgtgcgagcagagcgcgcgcataaactgccaagcatcaatt 1566
DB 1491 aagcaacggcccgagaggtgtgcgagcagagcgcgcgcataaactgccaagcatcaatt 1550

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QY 1567 aagcagaaggccatccctgacgagatggcccttttgcgtttctacaacctcttcctgctgc 1626
      |||
DB 1551 aagcagaaggccatccctgacgagatggcccttttgcgtttctacaacctcttcctgctgc 1610
QY 1627 atatctacaagccatccccacagatacgttaactagctcgtttttgcatcagaaga 1686
      |||
DB 1611 atatctacaagccatccccacagatacgttaactagctcgtttttgcatcagaaga 1670
QY 1687 gcagctat 1694
      |||
DB 1671 gcagctgt 1678

RESULT 12
AAQ83827
ID AAQ83827 standard; DNA: 5110 BP.
XX
AC AAQ83827;
XX
DT 04-OCT-1995 (first entry)
XX
DE Plasmid PCM-T297.
XX
KM Plasmid PCM-T297; bacteriophage T7; RNA polymerase:
XX mutant -116 to T; T7 promoter phi 10; circular; cyclic; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Promoter 198..220
FT /tag= a
FT /note= "Inactive T7 promoter phi 10 mutant (-116 to
      T) prior to a promoterless chloramphenicol
      acetyl transferase gene"
XX
PN US5385834-A.
XX
PD 31-JAN-1995.
XX
PF 13-AUG-1993; 93US-0106433.
XX
PR 13-AUG-1993; 93US-0106433.
XX
PA (GEOR-) GEORGIA TECH RES CORP.
XX
PI Ikeda RA:
XX
DR WPI: 1995-081565/11.
XX
PT New mutant form of T7 RNA polymerase - able to utilize a wide
PT range of T7 promoter sequences having mutations that inactivate
PT recognition by wild type enzyme
XX
PS Disclosure: Columns 57-62; 79pp; English.
XX
CC AAQ83827 is the plasmid PCM-T297, it was used in the production of
CC the bacteriophage T7 RNA polymerase mutant promoter phi 10 -116
CC to T substitution (claimed).
XX
SQ Sequence 5110 BP; 1305 A; 1288 C; 1288 G; 1229 T; 0 other;

Query Match 22.5%; Score 404; DB 16; Length 5110;
Best Local Similarity 96.5%; Pred. No. 4,9e-78;
Matches 413; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
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QY 1387 aggcataaataaagcgaagctcgaagactgggcttcgtttatctgtgtc 1446
      |||
DB 1371 aggcataaataaagcgaagctcgaagactgggcttcgtttatctgtgtc 1430
QY 1447 ttgtcgttgaagctctctctgtaagtaagaacaatcccggaagcgaattgaacgttgcg 1506
      |||
DB 1431 ttgtcgttgaagctctctctgtaagtaagaacaatcccggaagcgaattgaacgttgcg 1490
QY 1507 aagcaagcgccggaagggttgccggagcgagcgccgcacataaactggcgaagcatcaatt 1566
      |||
DB 1491 aagcaagcgccggaagggttgccggagcgagcgccgcacataaactggcgaagcatcaatt 1550
QY 1567 aagcagaaggccatccctgacgagatggcccttttgcgtttctacaacctcttcctgctgc 1626
      |||
DB 1551 aagcagaaggccatccctgacgagatggcccttttgcgtttctacaacctcttcctgctgc 1610
QY 1627 atatctacaagccatccccacagatacgttaactagctcgtttttgcatcagaaga 1686
      |||
DB 1611 atatctacaagccatccccacagatacgttaactagctcgtttttgcatcagaaga 1670
QY 1687 gcagctat 1694
      |||
DB 1671 gcagctgt 1678

RESULT 13
AAQ83828
ID AAQ83828 standard; DNA: 5110 BP.
XX
AC AAQ83828;
XX
DT 04-OCT-1995 (first entry)
XX
DE Plasmid PCM-P1160.
XX
KM Plasmid PCM-P1160; bacteriophage T7; RNA polymerase:
XX mutant -9C to G; T7 promoter phi 10; circular; cyclic; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Promoter 198..220
FT /tag= a
FT /note= "Inactive T7 promoter phi 10 mutant (-9C to
      G) prior to a promoterless chloramphenicol
      acetyl transferase gene"
XX
PN US5385834-A.
XX
PD 31-JAN-1995.
XX
PF 13-AUG-1993; 93US-0106433.
XX
PR 13-AUG-1993; 93US-0106433.
XX
PA (GEOR-) GEORGIA TECH RES CORP.
XX
PI Ikeda RA:
XX
DR WPI: 1995-081565/11.
XX
PT New mutant form of T7 RNA polymerase - able to utilize a wide
PT range of T7 promoter sequences having mutations that inactivate
PT recognition by wild type enzyme
XX
PS Disclosure: Columns 63-70; 79pp; English.
XX
CC AAQ83828 is the plasmid PCM-P1160, it was used in the production of
CC the bacteriophage T7 RNA polymerase mutant promoter phi 10 -9C
CC to G substitution (claimed).
XX
SQ Sequence 5110 BP; 1300 A; 1291 C; 1293 G; 1226 T; 0 other;
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```
XX US5385834-A.
PN
XX
XX 31-JAN-1995.
PD
XX
XX 13-AUG-1993: 93US-0106433.
PF
XX 13-AUG-1993: 93US-0106433.
PR
XX (GEOR-) GEORGIA TECH RES CORP.
PA
XX
XX Ikeda RA:
PI
XX WPI: 1995-081565/11.
DR
XX
XX New mutant form of T7 RNA polymerase - able to utilise a wide
PT range of T7 promoter sequences having mutations that inactivate
PT recognition by wild type enzyme
XX
PS Disclosure: Columns 77-83: 79pp: English.
XX
XX AA083830 is the plasmid pCM-P1087, it was used in the production of
CC the bacteriophage T7 RNA polymerase mutant promoter phl 10 -9C
CC to T substitution (claimed).
XX
SQ Sequence 5110 BP; 1305 A; 1287 C; 1289 G; 1229 T; 0 other:

Query Match      22.5%: Score 404; DB 16; Length 5110;
Best Local Similarity 96.5%; Pred. No. 4,9e-78;
Matches 413; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1267 agagtcgacctgcaagcatgcaagcttgggtcccaactgaccccatgacgaactcagaag 1326
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1251 agaatctgctcgcgagcagtagcgcggtggtcccaactgaccccatgacgaactcagaag 1310

QY 1327 tgaagcgccgtagcgccgagtagtgggtgtcccaactgacgaactgaggaactgccc 1386
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1311 tgaagcgccgtagcgccgagtagtgggtgtcccaactgacgaactgaggaactgccc 1370

QY 1387 aggcatacaataaagcaagagctcgaagagctgggcttgcgtttatctgtgtc 1446
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1371 aggcatacaataaagcaagagctcgaagagctgggcttgcgtttatctgtgtc 1430

QY 1447 ttgtcgggtgaagcctcctcgaagtagaacaatccgcgggagcggaattgaacgttgcg 1506
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1431 ttgtcgggtgaagcctcctcgaagtagaacaatccgcgggagcggaattgaacgttgcg 1490

QY 1507 aagcaacgcccggaggtgtgcgggcagagcccgccataaactgccaagcatcaaatc 1566
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1491 aagcaacgcccggaggtgtgcgggcagagcccgccataaactgccaagcatcaaatc 1550

QY 1567 aagcagaagagcctcctcgaagtagtgcttctgctttctacaactcttcctgtctc 1626
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1551 aagcagaagagcctcctcgaagtagtgcttctgctttctacaactcttcctgtctc 1610

QY 1627 atactacaagccatcccccacagatacggtaaactagcctcgttttgcatacagaaa 1686
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1611 atactacaagccatcccccacagatacggtaaactagcctcgttttgcatacagaaa 1670

QY 1687 gcagctatc 1694
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1671 gcagctgt 1678
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Search completed: September 12, 2002, 09:52:52
Job time: 686 sec